



## SEQUENCE LISTING

<110> GONG, Zhiyuan  
LAM, Toong Jin  
JU, Bensheng  
XU, Yanfei  
HE, Jiangyan  
YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF  
FLUORESCENT TRANSGENIC ORNAMENTAL FISH

<130> GLOF:007USC1

<140> 10/605,708

<141> 2003-10-22

<160> 24

<170> PatentIn Ver. 2.0

<210> 1

<211> 2480

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (90)..(1586)

<220>

<221> primer bind

<222> (66)..(85)

<223> CK2

<220>

<221> primer\_bind

<222> (97)..(120)

<223> CK1

<220>

<221> polyA signal

<222> (24467)..(2451)

<400> 1

ctctcctttg tgagcaacct cctccactca ctcctctctc agagagcact ctcgtacctc 60

cttctcagca actcaaagac acaggcatc atg tca acc agg tct atc tct tac 113

Met Ser Thr Arg Ser Ile Ser Tyr

1

5

tcc agc ggt ggc tcc atc agg agg ggc tac acc agc cag tca gcc tat 161

Ser Ser Gly Gly Ser Ile Arg Arg Gly Tyr Thr Ser Gln Ser Ala Tyr

10

15

20

gca gta cct gcc ggc tct acc agg atg agc tca gtg acc agt gtc agg 209

Ala Val Pro Ala Gly Ser Thr Arg Met Ser Ser Val Thr Ser Val Arg

25

30

35

40

aga tct ggt gtg ggt gcc agc cca ggc ttc ggt gcc ggt ggc agc tac	257
Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr	
45 50 55	
agc ttt agc agc agc agc atg ggt gga ggc tat gga agt ggt ctt ggt	305
Ser Phe Ser Ser Ser Ser Met Gly Gly Gly Tyr Gly Ser Gly Leu Gly	
gga ggt ctc ggt ggg ggc atg ggc ttt cgt tgc ggg ctt cct atc aca	353
Gly Gly Leu Gly Gly Gly Met Gly Phe Arg Cys Gly Leu Pro Ile Thr	
75 80 85	
gct gta act gtc aac cag aac ctg ttg gcc ccc tta aac ctg gaa atc	401
Ala Val Thr Val Asn Gln Asn Leu Leu Ala Pro Leu Asn Leu Glu Ile	
90 95 100	
gac ccc aca att caa get gtc cgc act tca gag aaa gag cag att aag	449
Asp Pro Thr Ile Gln Ala Val Arg Thr Ser Glu Lys Glu Gln Ile Lys	
105 110 115 120	
acc ttc aac aac cgc ttc get ttc ctc atc gac aaa gtg cgc ttc ctg	497
Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile Asp Lys Val Arg Phe Leu	
125 130 135	
gaa cag cag aac aag atg ctt gag acc aaa tgg agt ctt ctc caa gaa	545
Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Glu	
140 145 150	
cag aca acc aca cgt tcc aac atc gat gcc atg ttt gag gca tac atc	593
Gln Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala Tyr Ile	
155 160 165	
tct aac ctg cgc aga cag ctc gat gga ctg gga aat gag aag atg aag	641
Ser Asn Leu Arg Arg Gln Leu Asp Gly Leu Gly Asn Glu Lys Met Lys	
170 175 180	
ctg gag gga gag ctg aag aac atg cag ggc ctg gtt gag gac ttc aag	689
Leu Glu Gly Glu Leu Lys Asn Met Gln Gly Leu Val Glu Asp Phe Lys	
185 190 195 200	
aac aag tac gag gat gag atc aac aag cgt get tcc gta gag aat gag	737
Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Ala Ser Val Glu Asn Glu	
205 210 215	
ttt gtc ctg ctc aag aag gat gtt gat gca gcc tac atg aac aag gtt	785
Phe Val Leu Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Asn Lys Val	
220 225 230	
gag ctt gaa gcc aag gtt gat get ctt cag gat gag atc aac ttc ctc	833
Glu Leu Glu Ala Lys Val Asp Ala Leu Gln Asp Glu Ile Asn Phe Leu	
235 240 245	
agg gca gtc tac gag get gaa ctc cgg gag ctc cag tct cag atc aag	881
Arg Ala Val Tyr Glu Ala Glu Leu Arg Glu Leu Gln Ser Gln Ile Lys	
250 255 260	
gac aca tct gtt gtt gta gaa atg gac aac agc aga aac ctg gat atg	929

Asp Thr Ser Val Val Val Glu Met Asp Asn Ser Arg Asn Leu Asp Met	
265 270 275 280	
gac tcc atc gtg get gaa gtt cgc get cag tat gaa gac atc gcc aac	977
Asp Ser Ile Val Ala Glu Val Arg Ala Gln Tyr Glu Asp Ile Ala Asn	
285 290 295	
cgc agc cgt gcc gag gca gag agc tgg tac aaa cag aag ttt gag gag	1025
Arg Ser Arg Ala Glu Ala Glu Ser Trp Tyr Lys Gln Lys Phe Glu Glu	
300 305 310	
atg cag agc acc get ggt cag tat ggt gat gac ctc cgc tca aca aag	1073
Met Gln Ser Thr Ala Gly Gln Tyr Gly Asp Asp Leu Arg Ser Thr Lys	
315 320 325	
gct gag att get gaa ctc aac cgc atg atc gcc cgc ctg cag aac gag	1121
Ala Glu Ile Ala Glu Leu Asn Arg Met Ile Ala Arg Leu Gln Asn Glu	
330 335 340	
atc gat get gtc aag gca cag cgt gcc aac ttg gag get cag att get	1169
Ile Asp Ala Val Lys Ala Gln Arg Ala Asn Leu Glu Ala Gln Ile Ala	
345 350 355 360	
gag get gaa gag cgt gga gag ctg gca gtg aag gat gcc aag ctc cgc	1217
Glu Ala Glu Glu Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg	
365 370 375	
atc agg gag ctg gag gaa get ctt cag agg gcc aag caa gac atg gcc	1265
Ile Arg Glu Leu Glu Glu Ala Leu Gln Arg Ala Lys Gln Asp Met Ala	
380 385 390	
cgc cag gtc cgc gag tac cag gag ctc atg aac gtc aaa ttg get ctg	1313
Arg Gln Val Arg Glu Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu	
395 400 405	
gac att gag atc gcc acc tac agg aaa ctg ttg gaa gga gag gag agc	1361
Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser	
410 415 420	
aga ctg tcc agc ggt gga gct caa get acc att cat gtt cag cag acc	1409
Arg Leu Ser Ser Gly Gly Ala Gln Ala Thr Ile His Val Gln Gln Thr	
425 430 435 440	
tcc gga ggt gtt tca tct ggt tat ggt ggt agc ggc tct ggt ttc ggc	1457
Ser Gly Gly Val Ser Ser Gly Tyr Gly Ser Gly Ser Gly Phe Gly	
445 450 455	
tac agc agt ggc ttc agc agt ggt ggg tca gga tac ggt agt gga tca	1505
Tyr Ser Ser Gly Phe Ser Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser	
460 465 470	
gga ttc ggt tct gga tca ggg tat ggt gga ggc tcc atc agc aaa acc	1553
Gly Phe Gly Ser Gly Ser Gly Tyr Gly Gly Gly Ser Ile Ser Lys Thr	
475 480 485	
agt gtc acc acc gtc agc agt aaa cgc tat taa ggagaagcccc gcccaaacc	1606
Ser Val Thr Thr Val Ser Ser Lys Arg Tyr	

490

495

ccagccgaca cagtttccaa ccttccttac ctgcaactag atcccttctg aacctttctta 1666  
 cgactcaaac catctatggt gctatatattt agccagacag ctgtcccctg ttaatgagga 1726  
 gatgtggacg atgatttttta aagtacaaaa taagttttag attgttctgt gtgttgatgg 1786  
 tagttacccg tatcatgcat ctctgtctg gtggtgtcac tgccatttta aatcatcaac 1846  
 ccaactacac taaaacgata ccaggaagaa tcgtgtcca agccactgaa tagtcttatt 1906  
 tctgcactga tatgtacagg gaaagtgaga cacatagaaa ccactgtaac ctacgtagta 1966  
 ctatggtttc actggatcag ggggtgtgcta tacaagttcc tgaatgtctt gtttgaatgt 2026  
 tttgtgctgt tacaagctcc ctgctgtagt tttgctgact aatctgactt ttgtcatttt 2086  
 gctatggctg tcagagttgg tttacctatt ttctataaaa tgtatatggc agtcagccaa 2146  
 taactgatga caattgcttg tgggctacta atgtccagtt acctcacatt caagggagat 2206  
 ctgttacagc aaaaaacagg cacaatggga tttatgtgga ccatccctcc ttaaccttgt 2266  
 gtactttccg tgttggaaagt ggtgactgta ctgccttaca cattcccctg tattcaactg 2326  
 gcttccagag catattttac atccccggtt ataaatggaa aatgcaagaa aactgaaaca 2386  
 atgttcaacc agatttattt ggtattgatt gacgagacac caacttgaaa tttgaataca 2446  
 ataaatctga gaccacaaaa aaaaaaaaaa aaaa 2480

&lt;210&gt; 2

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Danio rerio

&lt;400&gt; 2

Met Ser Thr Arg Ser Ile Ser Tyr Ser Ser Gly Gly Ser Ile Arg Arg  
 1 5 10 15  
 Gly Tyr Thr Ser Gln Ser Ala Tyr Ala Val Pro Ala Gly Ser Thr Arg  
 20 25 30  
 Met Ser Ser Val Thr Ser Val Arg Arg Ser Gly Val Gly Ala Ser Pro  
 35 40 45  
 Gly Phe Gly Ala Gly Gly Ser Tyr Ser Phe Ser Ser Ser Ser Met Gly  
 50 55 60  
 Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly  
 65 70 75 80  
 Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Asn Leu Leu  
 85 90 95

Ala	Pro	Leu	Asn	Leu	Glu	Ile	Asp	Pro	Thr	Ile	Ala	Val	Arg	Thr	Ser		
			100					105					110				
Glu	Lys	Glu	Gln	Ile	Lys	Thr	Phe	Asn	Asn	Arg	Phe	Ala	Phe	Leu	Ile		
		115					120					125					
Asp	Lys	Val	Arg	Phe	Leu	Glu	Asn	Lys	Met	Leu	Glu	Thr	Lys	Trp	Ser		
	130					135					140						
Leu	Leu	Glu	Thr	Thr	Thr	Arg	Ser	Asn	Ile	Asp	Ala	Met	Phe	Glu	Ala		
145					150					155					160		
Tyr	Ile	Ser	Asn	Leu	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Asn	Glu	Lys	Met		
			165						170					175			
Lys	Leu	Glu	Gly	Glu	Leu	Lys	Asn	Met	Gln	Gly	Leu	Val	Glu	Asp	Phe		
		180					185						190				
Lys	Asn	Lys	Tyr	Glu	Asp	Glu	Ile	Asn	Lys	Arg	Ala	Ser	Val	Glu	Asn		
	195						200					205					
Glu	Phe	Val	Leu	Leu	Lys	Lys	Asp	Val	Asp	Ala	Ala	Tyr	Met	Asn	Lys		
	210					215					220						
Val	Glu	Leu	Glu	Ala	Lys	Val	Asp	Ala	Leu	Asp	Glu	Ile	Asn	Phe	Leu		
225					230					235					240		
Arg	Ala	Val	Tyr	Glu	Ala	Glu	Leu	Arg	Glu	Leu	Gln	Ser	Ile	Lys	Asp		
			245						250					255			
Thr	Ser	Val	Val	Val	Glu	Met	Asp	Asn	Ser	Arg	Asn	Leu	Asp	Met	Asp		
		260						265					270				
Ser	Ile	Val	Ala	Glu	Val	Arg	Ala	Gln	Tyr	Glu	Asp	Ile	Ala	Asn	Arg		
	275						280					285					
Ser	Arg	Ala	Glu	Ala	Glu	Ser	Trp	Tyr	Lys	Lys	Phe	Glu	Glu	Met	Gln		
	290					295					300						
Ser	Thr	Ala	Gly	Gln	Tyr	Gly	Asp	Asp	Leu	Arg	Ser	Thr	Lys	Ala	Glu		
305					310					315					320		
Ile	Ala	Glu	Leu	Asn	Arg	Met	Ile	Ala	Arg	Leu	Asn	Glu	Ile	Asp	Ala		
			325						330					335			
Val	Lys	Ala	Arg	Ala	Asn	Leu	Glu	Ala	Gln	Ile	Ala	Glu	Ala	Glu	Glu		
		340							345				350				
Arg	Gly	Glu	Leu	Ala	Val	Lys	Asp	Ala	Lys	Leu	Arg	Ile	Arg	Glu	Leu		
	355						360					365					
Glu	Glu	Ala	Leu	Gln	Arg	Ala	Lys	Asp	Met	Ala	Arg	Gln	Val	Arg	Glu		
	370					375					380						
Tyr	Gln	Glu	Leu	Met	Asn	Val	Lys	Leu	Ala	Leu	Asp	Ile	Glu	Ile	Ala		
385					390						395				400		

Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser Arg Leu Ser Ser Gly  
 405 410 415

Gly Ala Gln Ala Thr Ile His Val Gln Thr Ser Gly Gly Val Ser Ser  
 420 425 430

Gly Tyr Gly Gly Ser Gly Ser Gly Phe Gly Tyr Ser Ser Gly Phe Ser  
 435 440 445

Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser Gly Phe Gly Ser Gly Ser  
 450 455 460

Gly Tyr Gly Gly Gly Ser Ile Ser Lys Thr Ser Val Thr Thr Val Ser  
 465 470 475 480

Ser Lys Arg Tyr

<210> 3  
 <211> 1589  
 <212> DNA  
 <213> Danio rerio

<220>  
 <221> CDS  
 <222> (86)..(1231)

<220>  
 <221> primer\_bind  
 <222> (6)..(26)  
 <223> MCK2

<220>  
 <221> primer bind  
 <222> (20)..(38)  
 <223> MCK1

<220>  
 <221> polyA signal  
 <222> (1534)..(1539)

<400> 3  
 cctatttcgg cttggtgaac aggatctgat cccaaggact gttaccactt ttgttgtctt 60

ttgtgcagtg ttagaaaccg caatc atg cct ttc gga aac acc cac aac aac 112  
 Met Pro Phe Gly Asn Thr His Asn Asn  
 1 5

ttc aag ctg aac tac tca gtt gat gag gag tat cca gac ctt agc aag 160  
 Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys  
 10 15 20 25

cac aac aac cac atg gcc aag gtg ctg act aag gaa atg tat ggc aag 208  
 His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys  
 30 35 40

ctt agg gac aag cag acc cca cct gga ttc act gtg gat gat gtc atc 256

Leu	Arg	Asp	Lys	Gln	Thr	Pro	Pro	Gly	Phe	Thr	Val	Asp	Asp	Val	Ile	
			45					50					55			
cag	act	ggt	gtt	gac	aat	cca	ggc	cac	ccc	ttc	atc	atg	acc	gtc	ggc	304
Gln	Thr	Gly	Val	Asp	Asn	Pro	Gly	His	Pro	Phe	Ile	Met	Thr	Val	Gly	
		60					65					70				
tgt	gtt	gct	ggt	gat	gag	gag	tcc	tac	gat	gtt	ttc	aag	gac	ctg	ttc	352
Cys	Val	Ala	Gly	Asp	Glu	Glu	Ser	Tyr	Asp	Val	Phe	Lys	Asp	Leu	Phe	
	75					80					85					
gac	ccc	gtc	att	tcc	gac	cgt	cac	ggg	gga	tac	aag	gca	act	gac	aag	400
Asp	Pro	Val	Ile	Ser	Asp	Arg	His	Gly	Gly	Tyr	Lys	Ala	Thr	Asp	Lys	
	90				95					100					105	
cac	aag	acc	gac	ctc	aac	ttt	gag	aac	ctg	aag	ggg	ggg	gat	gac	ctg	448
His	Lys	Thr	Asp	Leu	Asn	Phe	Glu	Asn	Leu	Lys	Gly	Gly	Asp	Asp	Leu	
				110					115					120		
gac	ccc	aac	tac	ttc	ctg	agc	agc	cgt	gtg	cgt	acc	gga	cgc	agc	atc	496
Asp	Pro	Asn	Tyr	Phe	Leu	Ser	Ser	Arg	Val	Arg	Thr	Gly	Arg	Ser	Ile	
			125					130					135			
aag	gga	tac	ccc	ctg	ccc	ccc	cac	aac	agc	cgt	gga	gag	cgc	aga	gct	544
Lys	Gly	Tyr	Pro	Leu	Pro	Pro	His	Asn	Ser	Arg	Gly	Glu	Arg	Arg	Ala	
		140					145					150				
gtg	gag	aag	ctg	tct	gtt	gaa	gct	ctg	agt	agc	ttg	gat	gga	gag	ttc	592
Val	Glu	Lys	Leu	Ser	Val	Glu	Ala	Leu	Ser	Ser	Leu	Asp	Gly	Glu	Phe	
	155					160					165					
aag	ggc	aag	tac	tac	ccc	ctg	aag	tcc	atg	act	gat	gac	gag	cag	gag	640
Lys	Gly	Lys	Tyr	Tyr	Pro	Leu	Lys	Ser	Met	Thr	Asp	Asp	Glu	Gln	Glu	
	170				175					180					185	
cag	ctg	atc	gct	gac	cac	ttc	ctc	ttt	gac	aaa	ccc	gtc	tcc	ccc	ctg	688
Gln	Leu	Ile	Ala	Asp	His	Phe	Leu	Phe	Asp	Lys	Pro	Val	Ser	Pro	Leu	
				190					195					200		
ctg	ctg	gct	gct	ggt	atg	gcc	cgt	gac	tgg	ccc	gat	gcc	aga	ggc	att	736
Leu	Leu	Ala	Ala	Gly	Met	Ala	Arg	Asp	Trp	Pro	Asp	Ala	Arg	Gly	Ile	
			205					210					215			
tgg	cac	aat	gag	aac	aaa	gcc	ttc	ctg	gtc	tgg	gtg	aaa	cag	gag	gat	784
Trp	His	Asn	Glu	Asn	Lys	Ala	Phe	Leu	Val	Trp	Val	Lys	Gln	Glu	Asp	
		220					225					230				
cac	ctg	cgt	gtc	att	tcc	atg	cag	aag	ggg	ggc	aac	atg	aag	gaa	gtg	832
His	Leu	Arg	Val	Ile	Ser	Met	Gln	Lys	Gly	Gly	Asn	Met	Lys	Glu	Val	
	235					240					245					
ttc	aag	cgc	ttc	tgc	gtt	ggg	ctt	cag	agg	att	gag	gaa	att	ttc	aag	880
Phe	Lys	Arg	Phe	Cys	Val	Gly	Leu	Gln	Arg	Ile	Glu	Glu	Ile	Phe	Lys	
	250				255					260					265	
aag	cac	aac	cat	ggg	ttc	atg	tgg	aac	gag	cat	ctt	ggg	ttc	gtc	ctg	928
Lys	His	Asn	His	Gly	Phe	Met	Trp	Asn	Glu	His	Leu	Gly	Phe	Val	Leu	

270	275	280	
acc tgc ccc tcc aac ctg ggc aca ggc ctg cgc ggt gga gtc cac gtc			976
Thr Cys Pro Ser Asn Leu Gly Thr Gly Leu Arg Gly Gly Val His Val			
285	290	295	
aag ctg ccc aag ctc agc aca cat gcc aag ttt gag gag atc ctg acc			1024
Lys Leu Pro Lys Leu Ser Thr His Ala Lys Phe Glu Glu Ile Leu Thr			
300	305	310	
aga ctg cgc ctg cag aag cgt ggc aca ggg ggt gtg gac acc gct tcc			1072
Arg Leu Arg Leu Gln Lys Arg Gly Thr Gly Gly Val Asp Thr Ala Ser			
315	320	325	
gtt ggt gga gtg ttt gac att tcc aac gct gac cgt atc ggc tct tca			1120
Val Gly Gly Val Phe Asp Ile Ser Asn Ala Asp Arg Ile Gly Ser Ser			
330	335	340	345
gag gtt gag cag gtg cag tgt gtg gtt gat ggt gtc aag ctg atg gtg			1168
Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val			
350	355	360	
gag atg gag aag aag ctg gga gaa ggc cag tcc atc gac agc atg atc			1216
Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile			
365	370	375	
cct gcc cag aag taa agcgggaggc ccttccattt ttttcttcgt ctttgtctgt			1271
Pro Ala Gln Lys			
380			
ttttttacag tccaacagca acgsagagga aaactgctgc tcaaaaagac agtctcacct			1331
ttgcacctgt cttcttttcct ttttttccct tcttctctaa tttccatgtc atttcgccat			1391
ctttttttcc actttgtttc ctattaagtc ggtaacatct tgggatcaga taccggsgc			1451
aggagtgagt gcttgttgct gaggccttcac ctcaatttca gccttggttg taaaaagtga			1511
atcaatcaaa gttgtatttc aaaataaaaa tccccaataa aaaaaaaaaa aaaaaaaaaa			1571
aaaaaaaaaa aaaaaaaaaa			1589

<210> 4

<211> 381

<212> PRT

<213> Danio rerio

<400> 4

Met	Pro	Phe	Gly	Asn	Thr	His	Asn	Asn	Phe	Lys	Leu	Asn	Tyr	Ser	Val
1				5					10					15	
Asp	Glu	Glu	Tyr	Pro	Asp	Leu	Ser	Lys	His	Asn	Asn	His	Met	Ala	Lys
			20					25					30		
Val	Leu	Thr	Lys	Glu	Met	Tyr	Gly	Lys	Leu	Arg	Asp	Lys	Gln	Thr	Pro
		35					40					45			
Pro	Gly	Phe	Thr	Val	Asp	Asp	Val	Ile	Gln	Thr	Gly	Val	Asp	Asn	Pro
50						55					60				



Gly	His	Pro	Phe	Ile	Met	Thr	Val	Gly	Cys	Val	Ala	Gly	Asp	Glu	Glu	65	70	75	80
Ser	Tyr	Asp	Val	Phe	Lys	Asp	Leu	Phe	Asp	Pro	Val	Ile	Ser	Asp	Arg	85	90	95	
His	Gly	Gly	Tyr	Lys	Ala	Thr	Asp	Lys	His	Lys	Thr	Asp	Leu	Asn	Phe	100	105	110	
Glu	Asn	Leu	Lys	Gly	Gly	Asp	Asp	Leu	Asp	Pro	Asn	Tyr	Phe	Leu	Ser	115	120	125	
Ser	Arg	Val	Arg	Thr	Gly	Arg	Ser	Ile	Lys	Gly	Tyr	Pro	Leu	Pro	Pro	130	135	140	
His	Asn	Ser	Arg	Gly	Glu	Arg	Arg	Ala	Val	Glu	Lys	Leu	Ser	Val	Glu	145	150	155	160
Ala	Leu	Ser	Ser	Leu	Asp	Gly	Glu	Phe	Lys	Gly	Lys	Tyr	Tyr	Pro	Leu	165	170	175	
Lys	Ser	Met	Thr	Asp	Asp	Glu	Gln	Glu	Gln	Leu	Ile	Ala	Asp	His	Phe	180	185	190	
Leu	Phe	Asp	Lys	Pro	Val	Ser	Pro	Leu	Leu	Leu	Ala	Ala	Gly	Met	Ala	195	200	205	
Arg	Asp	Trp	Pro	Asp	Ala	Arg	Gly	Ile	Trp	His	Asn	Glu	Asn	Lys	Ala	210	215	220	
Phe	Leu	Val	Trp	Val	Lys	Gln	Glu	Asp	His	Leu	Arg	Val	Ile	Ser	Met	225	230	235	240
Gln	Lys	Gly	Gly	Asn	Met	Lys	Glu	Val	Phe	Lys	Arg	Phe	Cys	Val	Gly	245	250	255	
Leu	Gln	Arg	Ile	Glu	Glu	Ile	Phe	Lys	Lys	His	Asn	His	Gly	Phe	Met	260	265	270	
Trp	Asn	Glu	His	Leu	Gly	Phe	Val	Leu	Thr	Cys	Pro	Ser	Asn	Leu	Gly	275	280	285	
Thr	Gly	Leu	Arg	Gly	Gly	Val	His	Val	Lys	Leu	Pro	Lys	Leu	Ser	Thr	290	295	300	
His	Ala	Lys	Phe	Glu	Glu	Ile	Leu	Thr	Arg	Leu	Arg	Leu	Gln	Lys	Arg	305	310	315	320
Gly	Thr	Gly	Gly	Val	Asp	Thr	Ala	Ser	Val	Gly	Gly	Val	Phe	Asp	Ile	325	330	335	
Ser	Asn	Ala	Asp	Arg	Ile	Gly	Ser	Ser	Glu	Val	Glu	Gln	Val	Gln	Cys	340	345	350	
Val	Val	Asp	Gly	Val	Lys	Leu	Met	Val	Glu	Met	Glu	Lys	Lys	Leu	Gly	355	360	365	
Glu	Gly	Gln	Ser	Ile	Asp	Ser	Met	Ile	Pro	Ala	Gln	Lys				370	375	380	

<210> 5  
 <211> 1104  
 <212> DNA  
 <213> Danio rerio

<220>  
 <221> CDS  
 <222> (75)..(1034)

<220>  
 <221> primer bind  
 <222> (45)..(64)  
 <223> ARP2

<220>

<221> primer\_bind  
<222> (87)..(112)  
<223> ARK

<220>  
<221> polyA\_signal  
<222> (1069)..(1074)

<400> 5  
cgcgctcccta ccgtgagatt ttacaacctt gtctttaaac cggctgttca ccgataccttg 60  
gaagcactgc aaag atg ccc agg gaa gac agg gcc acg tgg aag tcc aac 110  
Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn  
1 5 10  
tat ttt ctg aaa atc atc caa ctg ctg gat gac ttc ccc aag tgt ttc 158  
Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe  
15 20 25  
atc gtg ggc gca gac aat gtc ggc tcc aag cag atg cag acc atc cgt 206  
Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg  
30 35 40  
ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg 254  
Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met  
45 50 55 60  
atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag 302  
Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu  
65 70 75  
agg ctg ctt ccc cac atc cgc ggg aac gtg ggc ttc gtc ttc acc aag 350  
Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys  
80 85 90  
gag gat ctg act gag gtc cga gac ctg ctg ctg gca aac aaa gtg ccc 398  
Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro  
95 100 105  
gct gct gcc cgt gct ggt gcc atc gcc ccc tgt gag gtg act gtg ccg 446  
Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro  
110 115 120  
gcc cag aac acc ggg ctc ggt cct gag aag acc tct ttc ttc cag gct 494  
Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala  
125 130 135 140  
ttg gga atc acc acc aag atc tcc aga gga acc att gaa atc ttg agt 542  
Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser  
145 150 155  
gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc 590  
Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala  
160 165 170  
acg ctg ctg aac atg ctg aac atg ctg aac atc tcg ccc ttc tcc tac 638  
Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr

175	180	185	
ggg ctg atc atc cag cag gtg tat gat aac ggc agt gtc tac agc ccc			686
Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro			
190	195	200	
gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag			734
Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys			
205	210	215	220
ggg gtg agg aac atc gcc agt gtg tgt ctg cag atc ggc tac cca act			782
Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr			
225	230	235	
ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg			830
Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu			
240	245	250	
gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg			878
Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val			
255	260	265	
aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt			926
Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val			
270	275	280	
gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag			974
Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu			
285	290	295	300
gca ccc aag gag gat tct gag gag tct gat gaa gac atg ggc ttc ggc			1022
Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly			
305	310	315	
ctg ttt gat taa accagacacc gaatatccat gtctgttttaa catcaataaa			1074
Leu Phe Asp			
320			
acatctggaa aaaaaaaaaa aaaaaaaaaa			1104

<210> 6  
 <211> 319  
 <212> PRT  
 <213> Danio rerio

<400> 2  
 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys  
 1 5 10 15  
 Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala  
 20 25 30  
 Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg  
 35 40 45  
 Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala  
 50 55 60  
 Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro  
 65 70 75 80

His	Ile	Arg	Gly	Asn	Val	Gly	Phe	Val	Phe	Thr	Lys	Glu	Asp	Leu	Thr
				85					90					95	
Glu	Val	Arg	Asp	Leu	Leu	Leu	Ala	Asn	Lys	Val	Pro	Ala	Ala	Ala	Arg
			100					105					110		
Ala	Gly	Ala	Ile	Ala	Pro	Cys	Glu	Val	Thr	Val	Pro	Ala	Gln	Asn	Thr
		115					120					125			
Gly	Leu	Gly	Pro	Glu	Lys	Thr	Ser	Phe	Phe	Gln	Ala	Leu	Gly	Ile	Thr
	130					135					140				
Thr	Lys	Ile	Ser	Arg	Gly	Thr	Ile	Glu	Ile	Leu	Ser	Asp	Val	Gln	Leu
145					150					155					160
Ile	Lys	Pro	Gly	Asp	Lys	Val	Gly	Ala	Ser	Glu	Ala	Thr	Leu	Leu	Asn
				165					170					175	
Met	Leu	Asn	Met	Leu	Asn	Ile	Ser	Pro	Phe	Ser	Tyr	Gly	Leu	Ile	Ile
			180					185					190		
Gln	Gln	Val	Tyr	Asp	Asn	Gly	Ser	Val	Tyr	Ser	Pro	Glu	Val	Leu	Asp
		195					200					205			
Ile	Thr	Glu	Asp	Ala	Leu	His	Lys	Arg	Phe	Leu	Lys	Gly	Val	Arg	Asn
	210					215					220				
Ile	Ala	Ser	Val	Cys	Leu	Gln	Ile	Gly	Tyr	Pro	Thr	Leu	Ala	Ser	Ile
225					230					235					240
Pro	His	Thr	Ile	Ile	Asn	Gly	Tyr	Lys	Arg	Val	Leu	Ala	Val	Thr	Val
				245					250					255	
Glu	Thr	Asp	Tyr	Thr	Phe	Pro	Leu	Ala	Glu	Lys	Val	Lys	Ala	Tyr	Leu
		260						265					270		
Ala	Asp	Pro	Thr	Ala	Phe	Ala	Val	Ala	Ala	Pro	Val	Ala	Ala	Ala	Thr
		275					280					285			
Glu	Gln	Lys	Ser	Ala	Ala	Pro	Ala	Ala	Lys	Glu	Glu	Ala	Pro	Lys	Glu
	290					295					300				
Asp	Ser	Glu	Glu	Ser	Asp	Glu	Asp	Met	Gly	Phe	Gly	Leu	Phe	Asp	
305					310					315					

<210> 7  
 <211> 2241  
 <212> DNA  
 <213> Danio rerio

<220>  
 <221> TATA signal  
 <222> (2103)..(2108)

<220>  
 <221> primer bind  
 <222> (2221)\_(2241)  
 <223> CK2

<220>  
 <221> misc feature  
 <222> (2142)..(2235)  
 <223> Identical to the 5' CK cDNA

<400> 7  
 ccttccttc tacttttgac gtccttttaa gattactcat ctcaaacacc catacaaagg 60  
 tcacacctgg tttatactat gatagttgta cagtgtggtg tgtgacaccc aactgtgtcc 120  
 aattgtctga ctatgcaggg tgtctatgct tatagtttac agttagacca aagtgtgtctg 180  
 gtgtgtgaag taacaaatga caaatactca aattgtaatt tactaagtag tttaaaaatg 240  
 tagtgcagtg ttggtacttt tatttcactt ttattcttgt ctatgtggat tagacaaatc 300

```

acatagaagg taaatcacat cataatgaac agcaaaactgt ttgccagcat taaaagaaga 360
agactgctta gatgcatgtc actgatgaga aaataaacttt aaacgcacac aagacggcac 420
gtacccaac gcagtgggga cgttgcat tgaactcaacg tcaggtcgat gtcaatgttc 480
ctaagtatgt tacagcttga tgttatgcgg ggattatggg tgccatacct gatgaataaa 540
ggttcgacat tggatttttg tcgctttcca cctatgacat cgttattgga cgtcaaaata 600
aatttaggtc accacaacct atatttaacc tgctgggcaa taactaaatg cactacagaa 660
taaatgcatc agctttttcac agcataatac aaaagctact tttcactcat actttgagta 720
acatttttag gcatgtattg atatttttac cagccctccc catacataat cgtatgttta 780
acattagctt tgttagccgc tagcattact gagcttggtc atgaaagcag atttgagct 840
gatgattgcc gtaccatgat ctcacacctt gacgattgcg taatgctatt aaatgcccat 900
atttcgtgtt gacttgcacg agaaatgaga tgggaacatt tatcagtggg cattaaatac 960
tatttttgtg tttagcttagc tgcagttttt aactattgta attaatgagt ttttctcaga 1020
tgtactttta ctttcccttg agtacatttt ccttccttca acctgcagtc actactttat 1080
agtccgtgta ttccctgtcca atcaaattgc taccttaaga catgggccat ttataattgc 1140
tgtcaaaaat atttacacgc attaacccag agatgatgga tgtttactgt atgatgaccg 1200
aagacgtcaa catggcggtta ggttgacgtt tgttttagaaa tgaaaattag gttgacgtca 1260
aacatccaat ctaaaatcat atatcaatgt atgttaccct tatgacgtct atcagacgtt 1320
tgtcattatt tgacgttggg ttaagatgtt acacaacct aatccaccaa atattaactt 1380
acaatatcct tagatgctgg ctagactttg taatattaac atcttatgat gttgtgtgcc 1440
tgttacgttt acacacatgt aaattacatg tcactactta ctactcttga gtacttttaa 1500
atattttaca ctgatacttt tactcgcact tatgattttt cagtactctt tccactactg 1560
cacatatggg ggagtttaga gccataatct gtgcagaatt gtgtgtgtgc acattttcca 1620
atatcaatac agaaggaaac tgtgttccct gttcccttgt aaatctcaac aatgcaactg 1680
ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaaaag tgaatggaaa 1740
aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa gagcagaggt 1800
taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca caccgctgg 1860
cagatgggtg gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
ctcaagctc tccttgcatc ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
caacatttat cttaccactt tctctctgta cctgtctaac aggtaggggtg tgtgtgagag 2040
tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccaccct ctcaagagtg 2100
tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
tgagcaacct cctccactca ctctctctc agagagcact ctctgtacct cttctcagca 2220
actcaaagac acaggatccg g
2241

```

```

<210> 8
<211> 1456
<212> DNA
<213> Danio rerio

```

```

<220>
<221> TATA signal
<222> (1389)..(1394)

```

```

<220>
<221> primer bind
<222> (1433)_(1456)
<223> MCK2

```

```

<220>
<221> misc feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA

```

```

<400> 8
gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
tgtggcctaa tcttggctga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
gcatgtgcac catgacaggc ctgttattca cacttggtgc catgttggag actgttcggc 180

```

```

cagctatagt tttcttcaca gagtcctggg tcacctaattg tcacaaggaa gaaacatggt 240
acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accagggagg ggttttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc ttaaaagaag 480
acacaacagg gatagttcac ccaaaaaaca gaccattctt tttttctggt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
aagtcaatgg gtcttccagc attttttcaa tataccttac tttgagttca aaagaaaaaac 660
acatctcaaa taggtttgag gttgaataaa catttttcat tttggggtgg actatcccta 720
attatttgac acttaagatt tatagtaaatt cattttatag acttttctcc cttattaaac 780
atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccttg 840
tcaaatgttt ttgtgtatgg ttggcgacaa atagactgaa ctggcctatc acacagactt 900
tcataacaac tccagttgat gccctttcac cctcagtgtg taaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaat gagtttgcac 1020
ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggctgacac 1080
gcgcacttct gatatctgtg gtatgtttgg caaaagtgtc gctcagcctt tttagcatgg 1140
cagatcctcc acatcccac acccctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260
catctaggat gcctggggcc taaattgaag cttttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttcagtgaac tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggta tatatatcca aatcaaactc ttcttgcttg ggtgaccctt atttcggctt 1440
ggtgaacagg atccgg                                     1456

```

```

<210> 9
<211> 2205
<212> DNA
<213> Danio rerio

```

```

<220>
<221> primer bind
<222> (2179)..(2205)
<223> ARP2

```

```

<220>
<221> misc_feature
<222> (2153)..(2199)
<223> Identical to the 5' ARP cDNA

```

```

<220>
<221> intron
<222> (792)..(2152)

```

```

<220>
<221> misc_feature
<222> (775)..(791)
<223> Identical to the 5' ARP cDNA

```

```

<400> 9
atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc 60
attttaattt gtgttgata attttacatt ttgtaagtat tatttttata aaaaatatat 120
agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180
gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
agataataaa gtgacttttt tgggcggacc aaatttcctt attaatggtc aattcattaa 360
aatacattca ttaaaataaaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagattt ttggctgttg ttagaaggga tacatctgcg gccgaaagtt aacgggaact 480

```

```

atttacattc tttgctatta aattatccat tatttgattt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatgc 600
tatattgacc gcagctgtat ccttttctaag tgcgactgta caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgacaca gatacgcat ttccgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctccttctc ttcacgcgtc 780
cctaccgtga ggtaaggctg acgccgctct tgtggcgggt tcttaaaatg tgtaataaaa 840
taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900
tatgcgttta aagcttggtg aatgattttt acagtaaaag ttagcactag cctgttagca 960
caggcctcgt gcgccatgtg tgacgcgacg ttttaatagc atcttatttg attttgatga 1020
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080
ttacatgcta gtacttggtc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140
ttttaaaacc agttactctc atttttagtga aatattctta agccactaag ttaaaaattg 1200
tcaatcacat ataattgtgt ttatgtttta tttgagtcac cataccaggc aatagtttta 1260
tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
gtaaaggtaa tcttaaaagg gttaaaggctc acccaaaaga caattcacgc tcaagtgttt 1380
tcaaatctta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560
tgcataaaatc agtttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620
gcagtggtca ccaagcttgt tcctgaaggg ccagtgctct acagatttta gctccaaccc 1680
taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740
gcaggtgtgt tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800
gtgacccctg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860
ttatggacag gctgttgcat tgcttggtcg tcgttccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcaggga cgctggtctc agacacgttt 1980
atagcagtaa atcaaatata atagtgtctc gattatcttt aaatatttga aagcttataa 2040
taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaat 2100
aagatgcaca caaggcagg gttaaaagtat tgcttggtgt tgtaatcctc agattttaca 2160
accttgtctt taaaccggct gttcaccgat ccttgggaagg gatcc 2205

```

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytokeratin - gene specific primer

<400> 10

cgctggagta agagatagac ctgg

24

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytokeratin gene specific primer

<220>

<221> misc feature

<222> (1)..(6)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (3)..(8)

<223> BamHI site

<400> 11

ccggatcctg tgtctttgag ttgctg

26

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Muscle creatine kinase gene specific primer

<220>

<221> misc feature

<222> (3)..(8)

<223> BamHI site

<400> 12

ccggatcctt gggatcagat cctg

24

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Muscle creatine kinase gene specific primer

<220>

<221> misc feature

<222> (1)..(3)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (3)..(B)

<223> BamHI site

<400> 13

ccggatcctg ttcaccaagc cgaa

24

<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer



<400> 14  
tagttggact tccacgtgcc ctgtc 25

<210> 15  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Acidic ribosomal protein PO gene specific primer

<220>  
<221> misc feature  
<222> (1)..(7)  
<223> Introduced for restriction site

<220>  
<221> misc feature  
<222> (1)..(6)  
<223> BamHI site

<400> 15  
ggatcccttc caaggatcgg tgaaca 26

<210> 16  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide for linker used in linker-mediated PCR

<400> 16  
gttcatcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c 51

<210> 17  
<211> 10  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide for linker used in linker-mediated PCR

<220>  
<223> n is a dideoxycytidine

<400> 17  
gaattcaagn 10

<210> 18  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
linker specific primer

<400> 18  
gttcattcttt acaagctagc g 21

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
linker specific primer

<400> 19  
tcctgaacaa tgctgtggac 20

<210> 20  
<211> 1392  
<212> DNA  
<213> Danio rerio

<220>  
<221> CDS  
<222> (42)..(551)

<220>  
<221> primer bind  
<222> (6)..(28)  
<223> M2

<220>  
<221> primer bind  
<222> (23)..(45)  
<223> M1

<220>  
<221> polyA signal  
<222> (797)..(802)

<220>  
<221> polyA\_signal <222> (1351)..(1357)

<400> 20  
ctcttcttga tcttctttaga cttcacacat accgtctcga c atg gca ccc aag aag 56  
Met Ala Pro Lys Lys  
1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104  
Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser  
10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152  
Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile  
25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200  
Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp  
40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248  
Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu  
55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296  
Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu  
70 75 80 85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344  
Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile  
90 95 100

gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392  
Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys  
105 110 115

aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440  
Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr  
120 125 130

gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488  
Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala  
135 140 145

ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536  
Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu  
150 155 160 165

gag aag gag gag taa acaaccttgg aatagaggaa acgaagagaa gaacatgcat 591  
Glu Lys Glu Glu  
170

cctcacagct taatctccag tctgttgtct ggccttctct aactttttgtt tttccttcct 651

ccctttcttg ctttctacca tcgttggttac tccaagcact tacactctcc atcttaccaa 711

agacttgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771

cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt 831

ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag 891

cttgcattga agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta 951

tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga 1011

```

aagaagcacg atggagtgat ctcaactctat aatagaggaa ccagtcatca ttctcatttc 1071
ctcctctgggt ggttgactaa aaagagaaaag agaaaatgag ggttttgtgc tgagtgagtt 1131
tagcctccta aaagcgatgc cgagctcatc acagagggag tgagagggac agaccatcct 1191
aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccct 1251
cctcttctct atttctctgt ccactctttt ttttttcttt tttctttttt gctttctgca 1311
tctgggcctg ctttgctctg ccaaacctct cctgtaacca ataaaaagac acaaactgtg 1371
aataaaaaaa aaaaaaaaaa a                                     1392

```

```

<210> 21
<211> 169
<212> PRT
<213> Danio rerio

```

```

<400> 21
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
 1          5          10          15
Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
          20          25          30
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
          35          40          45
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
          50          55          60
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
          65          70          75          80
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
          85          90          95
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
          100          105          110
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
          115          120          125
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
          130          135          140
Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
          145          150          155          160
Ile Thr His Gly Glu Glu Lys Glu Glu
          165

```

```

<210> 22
<211> 2054
<212> DNA
<213> Danio rerio

```

```

<220>
<221> TATA signal
<222> (1983)..(1989)
<220>

```

<221> enhancer  
<222> (142)..(148)  
<223> E-box, canntg

<220>  
<221> enhancer  
<222> (452)..(457)  
<223> E-box, canntg

<220>  
<221> enhancer  
<222> (1095)..(1100)  
<223> E-box, canntg

<220>  
<221> enhancer  
<222> (1278)..(1283)  
<223> E-box, canntg

<220>  
<221> enhancer  
<222> (1362)..(1367)  
<223> E-box, canntg

<220>  
<221> enhancer  
<222> (1385)..(1390)  
<223> E-box, canntg

<220>  
<221> enhancer  
<222> (523)..(532)  
<223> Potential MEF2 binding site, yta(w)4tar

<220>  
<221> enhancer  
<222> (606)..(615)  
<223> Potential MEF2 binding site, yta(w)4tar

<220>  
<221> enhancer  
<222> (697)..(706)  
<223> Potential MEF2 binding site, yta(w)4tar

<220>  
<221> enhancer  
<222> (1490)..(1499)  
<223> Potential MEF2 binding site, yta(w)4tar

<220>  
<221> enhancer  
<222> (1640)..(1649)  
<223> Potential MEF2 binding site, yta(w)4tar

<220>  
<221> enhancer  
<222> (1956)..(1965)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<223> Transcription start site at residue 2012

<220>

<221> primer bind

<222> (2032)..(2054)

<223> M2

<220>

<221> misc difference

<222> (2027)..(2054)

<223> Identical to the 5' MLC2f cDNA

<409> 22

```
tgcatgcctg gcaggccac tctagaggac tactagtcac atgcgattct gaacaatgct 60
ggaatgagcc accaactcat ccagtgtatt accctacact gggaaacacc caaatctgtc 120
tggtatattt gtgcatatac attagattag aagctgtcac tgcggtggta ccttttcaaa 180
ttgatacctc aaaagtatat attagtgcct tttaggtact aatatatacc cttgaggttt 240
tcatttggaag aggtaccacc ccagtgcag aaatctggag cttattttaac aaaataactt 300
tatttatatg ttattgaaaa atattaaata agcaaaacaa tggaaaaaaa ttagttcaaa 360
atttagcttt atttaaatgt ttttatcttt aatataagctg tttaataaat ctgttttgtt 420
actgagagat ggagaaaaat attcattttc ctgtaattat ctgtttttct aggtactgta 480
caagcaggag caaaacaagc cgacagactc ggaatgcac aacaaactca aggggggcaa 540
gagagcaagg agcgctcaag attgttttagc ctgccttccc aaaaaaaaac tgtcttaagc 600
caaccactca gagggctgta gtgtgctgac cgtgcttgct cacagggcag cttcccacaa 660
gtgaggtcac aggtcgatcg gcagagagag atgggcatgg ccatgtggac ggggtggtg 720
actatactag gaaaagcatt aaaacctatt aagacaccag aacgtcctct tatatatcag 780
tcattggctc aaaaatctct ggattgaaat atccaacaag taatcctgca agataagcca 840
ggagggagtg gcgtcccctt tagactcagt atgtgattgt atgaagctca aacagtcctt 900
gtggacagct tgaattcaat tcgccacaga ttttatgcag cggatgcca tccagttgca 960
ttttaaatta atatttttaa taggaagcta tcagtacact ctgagaaata aatgggtccg 1020
aggtacatat ttgtacttaa aggggtccata aaaaatttta agagaaacac ttttgtactt 1080
tattatggac ctttaaggta caaattttta ctacgcctt ttatttctga gagtgaagct 1140
atgataacgg tccaaaaact actacacca caaatttata aacaggggaa aatcaagaga 1200
attttagagt tgtaattttt ttgttgcaat caattttgtg actaaaatat tattttaata 1260
taaatgcacc aaaatacatt gcctatatc aaaaatgggt gtactcaatt actctaagca 1320
aaataatgct aatcttaaac aatttttgaa acaggatata aaattagtct aaagaaagaa 1380
aacagtgact gatgaattag acaagaaaaa tattttggtc accacagctg ttccttatgc 1440
ctcaaatttc tctcatgag ggtccaacat catctaaaaa ctgggaaaaa ggggtaatta 1500
atggcacctc acagtcaactg aagtgaccgg agagagagag agagagagag agtgctgaat 1560
ggggcacttg aaccgaaatc ttacagcatc ttcgattagg gctgatttga aataagggtt 1620
ccagggcgtg aacaaatatg aacaacataa ccatcaggat ctatcactgc aacctcccc 1680
gtattgatct gctgctaata taacttttagg ggctacagct cattcatttc aaattgagtt 1740
tacgtcccca tgccttatt agacaacgcg agacatgcag gccgctgcca tcagtatcag 1800
attcatccca ttccaagact ccaatagcta tttctgagca ctgtaagatg atagtacatc 1860
ccagccggtg tccctccatc actttcccc tacctcatag ttttctctct ttctctctcg 1920
gtctgctatt tcccaaacct cacttaaggt tgggtctata attagcaagg ggccttcgtc 1980
agtatataag cccctcaagt acaggacact acgcggttc agacttctct tcttgatctt 2040
cttagacttc acac 2054
```

<210> 23

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
MLC2F gene specific primer M1

<400> 23

ccatgtcgag acggtatgtg tga

23

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
MLC2F gene specific primer M2

<400> 24

gtgtgaagtc taagaagatc aag

23